IN THE CLAIMS

This listing of claims replaces all prior versions, and listings, in this application.

1. (currently amended) A modified polypeptide having carbohydrate processing enzymatic activity, said polypeptide comprising an amino acid sequence selected from:

(a) the amino acid sequence of SEQ ID NO:2 comprising a mutation in at least one of W433, E432 and M439;

(b) the amino acid sequence of a family 1 glycosyl hydrolase, comprising ~~at least one~~ a mutation at an amino acid residue ~~equivalent~~ corresponding to at least one of W433, E432 [[or]] and M439 of SEQ ID NO:2; and

(c) a variant of (a) ~~or (b)~~ having carbohydrate processing enzymatic activity and comprising ~~at least one~~ a mutation in an amino acid ~~mutation at a position equivalent to~~ residue corresponding to at least one of W433, E432 [[or]] and M439 of SEQ ID NO:2, wherein said variant has at least 30% identity to SEQ ID NO:2 over the entire length of the sequence or at least 30% identity to SEQ ID NO:2 over the region from residue 425 to residue 450 of SEQ ID NO:2.

2. (original) The polypeptide according to claim 1 in which the mutation is selected to broaden the substrate specificity of the polypeptide compared to a polypeptide not so modified.

3. (original) The polypeptide according to claim 1, wherein the mutation is an amino acid substitution.

4. (currently amended) The polypeptide according to claim 1 in which the polypeptide comprises:

(i) SEQ ID NO:2 having one or more of W433, E 432 and M439 substituted by cysteine, valine or alanine; or

(ii) the amino acid sequence as defined in (b) or (c) having one or more of the amino acid residues ~~equivalent~~ corresponding to W433, E432 [[or]] and M439 of SEQ ID NO:2 substituted by cysteine, valine or alanine.

5. (currently amended) A modified polypeptide having carbohydrate processing enzymatic activity, said polypeptide comprising an amino acid sequence selected from:

(a) the amino acid sequence of SEQ ID NO:2 comprising one or more mutations selected from the group consisting of W433C, E432C and M439C;

(b) the amino acid sequence of a family 1 glycosyl hydrolase, comprising ~~at least one~~ a mutation [[at]] in an amino acid ~~equivalent~~ residue corresponding to at least one of W433, E432 [[or]] and M439 [[in]] of SEQ ID NO:2 wherein the amino acid is substituted by a C (cysteine) residue; and

(c) a variant of (a) ~~or (b)~~ having carbohydrate processing enzymatic activity and comprising ~~at least one~~ a mutation [[at]] in an amino acid ~~equivalent to~~ residue corresponding to at least one of W433, E432 [[or]] and M439 [[in]] of SEQ ID NO:2 wherein the amino acid is substituted by a C (cysteine) residue and wherein said variant has at least 30% identity to SEQ ID NO:2 over the entire length of the sequence or at least 30% identity to SEQ ID NO:2 over the region from residue 425 to residue 450 of SEQ ID NO:2.

6. (original) The polypeptide according to claim 5, wherein the C residue introduced by the mutation is chemically modified.

7. (original) The polypeptide according to claim 6, wherein the C residue is modified so as to comprise a positively-charged group.

8. (original) The polypeptide according to claim 7, wherein the positively charged group is of formula $-(CH_2)n-N^+R_3$, wherein n is a positive integer from 1 to 4 and each R, which may be the same or different, is H or a C_1-C_4 alkyl group.

9. (original) The polypeptide according to claim 8, wherein the positively charged group is $-CH_2CH_2NMe_3^+$.

10. (original) The polypeptide according to claim 6, wherein the C residue is modified so as to comprise a negatively-charged group.

11. (original) The polypeptide according to claim 10, wherein the negatively-charged group is of formula $-(CH_2)n-SO_3^-$ or $-(CH_2)n-COO^-$, wherein n is a positive integer from 1 to 4.

12. (original) The polypeptide according to claim 11, wherein the negatively-charged group is of formula $-(CH_2)n-SO_3^-$.

13. (original) The polypeptide according to claim 6, wherein the C residue is modified so as to comprise an uncharged group.

14. (original) The polypeptide according to claim 13, wherein the uncharged group is a C_1-C_4 alkyl group.

15. (original) The polypeptide according to claim 14, wherein the uncharged group is methyl.

16. (original) The polypeptide according to claim 1, which further comprises a mutation of a catalytic nucleophilic residue of the active site.

17. (currently amended) The polypeptide according to claim 16, wherein the further mutation is:

(i) E387A or E387G in SEQ ID NO:2 or

(ii) substitution ~~of E387~~ with A or G at the amino acid residue corresponding to E387 of SEQ ID NO:2 in the amino acid sequence as defined in (b) or (c) of claim 1.

18. (original) The polypeptide according to claim 1, wherein the polypeptide has glycosyl synthase, glycosyl hydrolase, and/or transglycosylase activity.

19. (original) The polypeptide according to claim 1, wherein the family 1 glycosyl hydrolase is *Sulfolobus solfataricus* β-glycosidase.

20. (original) The polypeptide according to claim 6, which further comprises a mutation of a catalytic nucleophilic residue of the active site.

21. (currently amended) The polypeptide according to claim 20, wherein the further mutation is:

(i) E387A or E387G in SEQ ID NO:2 or

(ii) substitution ~~of E387~~ with A or G at the amino acid residue corresponding to E387 of SEQ ID NO:2 in the amino acid sequence as defined in (b) or (c) of claim 5.

22. (original) The polypeptide according to claim 6, wherein the polypeptide has glycosyl synthase, glycosyl hydrolase, and/or transglycosylase activity.

23. (original) The polypeptide according to claim 6, wherein the family 1 glycosyl hydrolase is *Sulfolobus solfataricus* β-glycosidase.

Claims 24-26 (canceled)

27. (withdrawn/currently amended) A method for hydrolysing a β-glycoside, synthesising a β-glycoside or transglycosylation, which method comprises contacting a glycoside

substrate with a modified polypeptide having carbohydrate processing enzymatic activity, said polypeptide comprising an amino acid sequence selected from:

(a) the amino acid sequence of SEQ ID NO:2 comprising a mutation in at least one of W433, E432 [[or]] and M439;

(b) the amino acid sequence of a family 1 glycosyl hydrolase, comprising ~~at least one~~ a mutation [[at]] in an amino acid residue ~~equivalent~~ corresponding to at least one of W433, E432 [[or]] and M439 of SEQ ID NO:2; and

(c) a variant of (a) ~~or (b)~~ having carbohydrate processing enzymatic activity and comprising ~~at least one~~ a mutation in an amino acid ~~mutation at a position equivalent to~~ residue corresponding to at least one of W433, E432 [[or]] and M439 of SEQ ID NO:2, wherein said variant has at least 30% identity to SEQ ID NO:2 over the entire length of the sequence or at least 30% identity to SEQ ID NO:2 over the region from residue 425 to residue 450 of SEQ ID NO:2.

28. (withdrawn) The method according to claim 27, wherein the glycoside substrate is selected from the group consisting of a glucoside, a galactoside, a fucoside, a xyloside, a mannoside, and a glucuronide.

29. (withdrawn) The method according to claim 27, wherein the polypeptide is contacted with a sample containing at least two different glycosides.

30. (withdrawn/currently amended) A method for hydrolysing a β-glycoside, synthesising a β-glycoside or transglycosylation, which method comprises contacting a glycoside substrate with a modified polypeptide having carbohydrate processing enzymatic activity, said polypeptide comprising an amino acid sequence selected from:

(a) the amino acid sequence of SEQ ID NO:2 comprising one or more mutations selected from the group consisting of W433C, E432C and M439C;

(b) the amino acid sequence of a family 1 glycosyl hydrolase, comprising ~~at least one~~ a mutation [[at]] in an amino acid ~~equivalent~~ corresponding to at least one of

W433, E432 [[or]] and M439 [[in]] of SEQ ID NO:2 wherein the amino acid is substituted by a C (cysteine) residue; and

(c) a variant of (a) ~~or (b)~~ having carbohydrate processing enzymatic activity and comprising ~~at least one~~ a mutation [[at]] in an amino acid ~~equivalent to~~ residue corresponding to at least one of W433, E432 [[or]] and M439 [[in]] of SEQ ID NO:2 wherein the amino acid is substituted by a C (cysteine) residue, wherein said variant has at least 30% identity to SEQ ID NO:2 over the entire length of the sequence or at least 30% identity to SEQ ID NO:2 over the region from residue 425 to residue 450 of SEQ ID NO:2; and

wherein the C residue introduced by the mutation of (a), (b) or (c) is chemically modified.

31. (withdrawn) The method according to claim 30, wherein the glycoside substrate is selected from the group consisting of a glucoside, a galactoside, a fucoside, a xyloside, a mannoside, and a glucuronide.

32. (withdrawn) The method according to claim 30, wherein the polypeptide is contacted with a sample containing at least two different glycosides.

33. (new) The polypeptide according to claim 1, wherein the variant (c) has at least 50% identity to SEQ ID NO:2 over the entire length of the sequence or at least 50% identity to SEQ ID NO:2 over the region from residue 425 to residue 450 of SEQ ID NO:2.

34. (new) The polypeptide according to claim 33, wherein the variant (c) has at least 65% identity to SEQ ID NO:2 over the entire length of the sequence or at least 65% identity to SEQ ID NO:2 over the region from residue 425 to residue 450 of SEQ ID NO:2.

35. (new) The polypeptide according to claim 34, wherein the variant (c) has at least 80% identity to SEQ ID NO:2 over the entire length of the sequence or at least 80%

identity to SEQ ID NO:2 over the region from residue 425 to residue 450 of SEQ ID NO:2.

36. (new) The polypeptide according to claim 35, wherein the variant (c) has at least 90% identity to SEQ ID NO:2 over the entire length of the sequence or at least 90% identity to SEQ ID NO:2 over the region from residue 425 to residue 450 of SEQ ID NO:2.

37. (new) The polypeptide according to claim 36, wherein the variant (c) has at least 95% identity to SEQ ID NO:2 over the entire length of the sequence or at least 95% identity to SEQ ID NO:2 over the region from residue 425 to residue 450 of SEQ ID NO:2.

38. (new) The polypeptide according to claim 37, wherein the variant (c) has at least 99% identity to SEQ ID NO:2 over the entire length of the sequence.

39. (new) The polypeptide according to claim 1, said polypeptide comprising the amino acid sequence of a family 1 glycosyl hydrolase, comprising a mutation in an amino acid residue corresponding to at least one of W433, E432 and M439 of SEQ ID NO:2.

40. (new) The polypeptide according to claim 39 wherein said mutation consists of substitution of the amino acid residue corresponding to at least one of W433, E432 and M439 of SEQ ID NO: 2 by cysteine, valine or alanine.

41. (new) The polypeptide according to claim 1, said polypeptide comprising an amino acid sequence selected from:

(a) the amino acid sequence of SEQ ID NO:2 comprising a mutation in at least one of W433, E432 and M439; and

(b) the amino acid sequence of a family 1 glycosyl hydrolase, comprising a mutation at an amino acid residue corresponding to at least one of W433, E432 and M439 of SEQ ID NO:2;

wherein said polypeptide further comprises a mutation of a catalytic nucleophilic residue of the active site.